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In the Specification:

Please replace the paragraph beginning at page 8, line 16 with the following rewritten paragraph:

--A "CI-2 like" polypeptide refers to a polypeptide of at least 23 consecutive amino acids of Seq. ID No. 2 or 4; or a polypeptide of at least 30% amino acid sequence identity with corresponding region of Seq. ID Nos. 2 or 4 or 20; or a CI-2-like polypeptide with modifications identified in CI-2; or a protease inhibitor with an active site loop typically between 53 and 70; or a CI-2 homologue modified to enhance its nutritional value by altering the amino acid residues at positions corresponding to those defined herein. The following organisms may be modified according to the methods and figures in the specification: *Hordeum vulgare, Zea mays, Vicia faba, Cucurbita maxima, Canavalia lineata, Vigna angularis, Nicotiana tabacum, Nicotiana sylvestris, Sambucus nigra, Momordica charantia, Solanum tuberosum, Lycopersicon peruvianum, Lycopersicon esculentum, Amaranthus caudatus, Arabidopsis thalania.*--

Please replace the paragraph beginning at page 5, line 19 with the following rewritten paragraph:

Figure 2 - CI-2-like sequences

1. Seq. ID No. 35, Hordeum vulgare (gi:68800)
2. Seq. ID No. 36,Hordeum vulgare (Y08625)
3. Seq. ID No. 37, Zea mays (gi:475922) -
4. Seq. ID No. 38, Vicia faba (A21463)
5. Seq. ID No. 39, Cucurbita maxima (S55591, S12897)
6. Seq. ID No. 40, Canavalia lineata (JC2380)
7. Seq. ID No. 41, Vigna angularis (JX0089)
8. Seq. ID No. 42, Nicotiana tabacum (gi:19913)

9. Seq. ID No. 43, Nicotiana sylvestris (A56555)
10. Seq. ID No. 44, Sambucus nigra (Z46949)
11. Seq. ID No. 45, Momordica charantia (JC2508)
12. Seq. ID No. 46, Cucurbita maxima (S12897)
13. Seq. ID No. 47, Solanum tuberosum (P01052,_U30861)
14. Seq. ID No. 48, Solanum tuberosum (U30861)
15. Seq. ID No. 49, Lycopersicon peruvianum (A39547)
16. Seq. ID No. 50, Lycopersicon esculentum (A32067, A24048)
17. Seq. ID No. 51, Lycopersicon esculentum (A24048)
18. Seq. ID No. 52, Amaranthus caudatus (S40496)
19. Seq. ID No. 53, Arabidopsis thalania (AC005770)
20. Seq. ID No. 33, consensus sequence
22. Seq. ID No. 34, consensus sequence

Please replace the paragraphs beginning at page 49, line 25 through paragraph beginning at page 54, line 6 with the following rewritten paragraphs:

BHL1

The BHL1 insert corresponds to SEQ ID NO 5. Oligonucleotide pairs, N4394 (Seq ID NO. 54)/N4395 (Seq ID NO. 55), and N4396 (Seq ID NO. 56)/N4397 (Seq ID NO. 57), were annealed and ligated together to make a 202 base pair double stranded DNA molecule with overhangs compatible with *Rca* I and *Nhe* I restriction sites. PCR was performed on the annealed molecule using primers N5045 (Seq ID NO. 58) and N5046 (Seq ID NO. 59) to add a 5' *Spe* I site and 3' *Hind* III site. The PCR product was then restriction digested at those sites and ligated into pBluescript II KS+ at *Spe* I and *Hind* III sites. The insert was then removed by restriction digestion with *Rca* I and *Hind* III and was ligated into the *Nco* I and *Hind* III sites of pET28a (Novagen) to form the BHL1 construct.

Oligonucleotide sequences (5' to 3'):

N4394 (Seq ID NO. 54)

1 CATGAAGCTG AAGACAGAGT GGCCGGAGTT GGTGGGGAAA TCGGTGGAGA

51 AAGCCAAGAA GGTGATCCTG AAGGACAAGC CAGAGGCGCA
AATCATAGTT
101 CTGC

N4395 (Seq ID NO. 55)

1 CAACCGGCAG AACTATGATT TGCGCCTCTG GCTTGTCCTT
CAGGATCACC
51 TTCTTGGCTT TCTCCACCGA TTTCCCCACC AACTCCGGCC
ACTCTGTCTT
101 CAGCTT

E4 cont.

N4396 (Seq ID NO. 56)

1 CGGTTGGTAC AAAGGTGACG AAGGAATATA AGATCGACCG
CGTCAAGCTC
51 TTTGTGGATA AAAAGGACAA CATCGCGCAG GTCCCCAGGG TCGG

N4397 (Seq ID NO. 57)

1 CTAGCCGACC CTGGGGACCT GCGCGATGTT GTCCTTTTTA
TCCACAAAGA
51 GCTTGACGCG GTCGATCTTA TATTCCTTCG TCACCTTTGT AC

N5045 (Seq ID NO. 58)

1 GTACTAGTCA TGAAGCTGAA GACAGA

N5046 (Seq ID NO. 59)

GAGAAGCTTG CTAGCCGACC CTGGGGAC

BHL2

The BHL2 construct insert corresponds to SEQ ID NO 7. An overlap PCR strategy was used to make the BHL2 construct. PWO polymerase from Boehringer-Mannheim was used for all PCR reactions. The primers were chosen to change 3 amino acids in the BHL1 active site loop region, and to create unique *Age* I and *Hind* III restriction sites flanking the active site loop, to facilitate loop replacement in future constructs. A unique *Rca* I site (compatible with *Nco* I) was included at the 5'

end, and a unique *Xho* I site was included at the 3' end. The overlap PCR was done as follows: PCR was done with primers N13561 (Seq. Id No. 60) and N13564 (Seq. Id No. 63), using the BHL1 construct as template. A separate PCR was done with primers N13563 (Seq. Id No. 62) and N13562 (Seq. Id No. 61) again using the BHL1 construct as template. The products from both reactions were gel purified and combined. Primer N13565 (Seq. Id No. 64), which overlapped regions on both of the PCR products, was then added and another PCR was done to generate the full-length insert. The resulting product was amplified by another PCR with primers N13561 (Seq. Id No. 60) and N13562 (Seq. Id No. 61). It was subsequently suspected that a deletion was present in N13562 (Seq. Id No. 61) that caused a frameshift near the 3' end of the PCR product. To avoid this frameshift problem, a final PCR reaction was done with primers N13562 (Seq. Id No. 61) and N13905 (Seq. Id No. 65). The final PCR product was digested with *Rca* I and *Xho* I, and then ligated into the *Nco* I and *Xho* I sites of pET 28b. Note: Some primers had 6-oligonucleotide extensions to improve restriction digestion efficiency.

E4 cont.

Oligonucleotide sequences (5' TO 3'):

N13561 (Seq. Id No. 60)

1 TTTTTTTCATGAAGCTGAAGACA

N13562 (Seq. Id No. 61) (as ordered)

1 TTTTTTCTCGAGGCTAGCCGACCCTGGGGA

N13563 (Seq. Id No. 62)

1 ATCGACAAGGTCAAGCTTTTTGTGGATAAAAAGGA

N13564 (Seq. Id No. 63)

1 CACCTTTGTACCAACCGGTAGAACTATGATTTGCGC

N13565 (Seq. Id No. 64)

1 GTTGGTACAAAGGTGGCGAAGGCCTATAAGATCGACAAGGTCAAG

N13905 (Seq. Id No. 65)

1 TTTTTTCTCGAGGCTAGCCGACCCTGGGGACCTGCGCTA

BHL3

The BHL3 construct insert corresponds to SEQ ID NO 9. The BHL2 construct was digested with *Age* I and *Hind* III, and the region between these sites was removed by gel purification and discarded. Oligonucleotide pairs, N14471 (Seq. Id No. 66) and N14472 (Seq. Id No. 67), were annealed to make a double stranded DNA molecule with overhangs compatible with *Age* I and *Hind* III restriction sites. The annealed product was ligated into the *Age* I and *Hind* III sites of the digested BHL2 construct to yield the BHL3 construct.

E4 cont.

Oligonucleotide sequences (5' to 3'):

N14471 (Seq. Id No. 66)

1 CCGGTTGGTACAAAGGTGGGTAAGCATTATAAGATCGACAAGGTCA

N14472 (Seq. Id No. 67)

AGCTTGACCTTGTCGATCTTATAATGCTTACCCACCTTTGTACCAA

BHL3N

The BHL3N construct insert corresponds to SEQ ID No 11. A PCR reaction was done with the BHL3 construct as template. The primers for this reaction were N13771 (Seq. Id No. 68) and N13905 (Seq. Id No. 65). The resulting PCR product was digested with *Rca* I and *Xho* I and ligated into the *Nco* I and *Xho* I sites of pET 28b to yield the BHL3N construct.

Oligonucleotide sequences (5' to 3'):

N13771 (Seq. Id No. 68)

1

TTTTTTTCATGAAGTCGGTGGAGAAGAAACCGAAGGGTGTGAAGACAGGTGCG

GGTGACAAGCATAAGCTGAAGACAGAGTG

N13905 (Seq. Id No. 65) (already provided in BHL2 description).

BHL4

The BHL4 construct insert DNA corresponds to SEQ ID NO 13. The BHL2 construct was digested with *Age* I and *Hind* III, and the region between these sites was removed by gel purification and discarded. Oligonucleotide pairs, N22098 (Seq. Id No. 69) and N22099 (Seq. Id No. 70), were annealed to make a double stranded DNA molecule with overhangs compatible with *Age* I and *Hind* III restriction sites. The annealed product was ligated into the *Age* I and *Hind* III sites of the digested BHL2 construct to yield the BHL4 construct.

E4 cont.

Oligonucleotide sequences (5' to 3'):

N22098 (Seq. Id No. 69)

CCGGTTGGTACAAAGGTGACGGGCGAATACAAGATCGACCGCGTCA

N22099 (Seq. Id No. 70)

AGCTTGACGCGGTCGATCTTGTATTCGCCCGTCACCTTTGTACCAA

BHL5

The BHL5 construct insert DNA corresponds to SEQ ID NO 15. This gene was synthesized by a commercial vendor, The Midland Certified Reagent Company (Midland, Texas). The gene was supplied by Midland following digestion by *Nco* I and *Hind* III, and was ligated into the *Nco* I and *Hind* III sites of pET 28b to yield the BHL5 construct.

BHL6

The BHL6 construct insert DNA corresponds to SEQ ID NO 17. The BHL5 construct was digested with *Age* I and *Sal* I, and the region between these sites was removed by gel purification and discarded. Oligonucleotide pairs, N23923 (Seq. Id No. 71) and N23924 (Seq Id. No 72), were annealed to make a double stranded DNA molecule with overhangs compatible with *Age* I and *Sal* I restriction sites. The annealed product was ligated into the *Age* I and *Sal* I sites of the digested BHL5 construct to yield the BHL6 construct.

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Oligonucleotide sequences (5' to 3'):

N23923 (Seq. Id No. 71)

CCGGTGAATGGAAGATGGATCGCGTCCGCCTCTGGG

E4 cont.

N23924 (Seq Id. No 72)

TCGACCCAGAGGCGGACGCGATCCATCTTCCATTCA

BHL8

The BHL8 construct insert DNA corresponds to SEQ ID No 19. A PCR reaction was done using the BHL6 construct as template. The primers for this reaction were N26671 (Seq ID. No 73) and N26672 (Seq ID. No 74). The resulting PCR product was digested with *Nco* I and *Hind* III and ligated into the *Nco* I and *Hind* III sites of pET 28b to yield the BHL8 construct.

Oligonucleotide sequences (5' to 3'):

N26671 (Seq ID. No 73)

TTTTTTCCATGGCTAAGATGAAGTGCACGTGGCCTGAGCTGGT

N26672 (Seq ID. No 74)

TTTTTTAAGCTTGGATCCCTAGCCGCACTTCGGAGTCTTGGCGA